



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: French, Cynthia K.  
Schneider, Patrick A.  
Yamamoto, Karen K.

(ii) TITLE OF INVENTION: Prostate Cancer-Specific Marker

(iii) NUMBER OF SEQUENCES: 2

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
(B) STREET: Two Embarcadero Center, 8th Floor  
(C) CITY: San Francisco  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94111

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: (to be assigned)  
(B) FILING DATE: (herewith)  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dow, Karen B.  
(B) REGISTRATION NUMBER: 29,684  
(C) REFERENCE/DOCKET NUMBER: 018002-000210US

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-576-0200  
(B) TELEFAX: 415-576-0300

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 3891 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

10

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 151..1425

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCTTTGCCT CCTCCCTGTT CCAGGAGCTG GTGCCCTGGG CTCTGCGCTG TTGTTTTTCAG 60  
 20 CGTTCCGAAA GCCGGCGCTT GAGATCCAGG CAAGTGAATC CAGCCAGGCA GTTTTCCCTT 120  
 CAGCACCTCG GACAGAACAC GCAGTAAAAA ATG GCT CCG ATC ACC ACC AGC CGG 174  
 Met Ala Pro Ile Thr Thr Ser Arg  
 1 5  
 25 GAA GAA TTT GAT GAA ATC CCC ACA GTG GTG GGG ATC TTC AGT GCA TTT 222  
 Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe  
 10 15 20  
 30 GGC CTG GTC TTC ACA GTC TCT CTC TTT GCA TGG ATC TGC TGT CAG AGA 270  
 Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln Arg  
 25 30 35 40  
 35 AAA TCA TCC AAG TCT AAC AAG ACT CCT CCA TAC AAG TTT GTG CAT GTG 318  
 Lys Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val  
 45 50 55  
 40 CTT AAG GGA GTT GAT ATT TAC CCT GAA AAC CTA AAT AGC AAA AAG AAG 366  
 Leu Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys  
 60 65 70  
 TTT GGA GCA GAT GAT AAA AAT GAA GTA AAG AAT AAG CCA GCT GTG CCA 414  
 Phe Gly Ala Asp Asp Lys Asn Glu Val Lys Asn Lys Pro Ala Val Pro  
 75 80 85  
 45 AAG AAT TCA TTG CAT CTG GAT CTT GAA AAG AGA GAT CTC AAT GGC AAT 462  
 Lys Asn Ser Leu His Leu Asp Leu Glu Lys Arg Asp Leu Asn Gly Asn  
 90 95 100  
 50 TTT CCC AAA ACC AAC CTC AAA CCT GGC AGT CCT TCT GAT CTG GAG AAT 510  
 Phe Pro Lys Thr Asn Leu Lys Pro Gly Ser Pro Ser Asp Leu Glu Asn  
 105 110 115 120  
 55 GCA ACC CCG AAG CTC TTT TTA GAA GGG GAA AAA GAG TCA GTT TCC CCT 558  
 Ala Thr Pro Lys Leu Phe Leu Glu Gly Glu Lys Glu Ser Val Ser Pro  
 125 130 135  
 60 GAG AGT TTA AAG TCC AGC ACT TCC CTT ACT TCA GAA GAG AAA CAA GAG 606  
 Glu Ser Leu Lys Ser Ser Thr Ser Leu Thr Ser Glu Glu Lys Gln Glu  
 140 145 150  
 AAG CTG GGA ACT CTC TTC TTC TCC TTA GAA TAC AAC TTC GAG AGA AAA 654  
 Lys Leu Gly Thr Leu Phe Phe Ser Leu Glu Tyr Asn Phe Glu Arg Lys  
 155 160 165  
 65 GCA TTT GTG GTC AAT ATC AAG GAA GCC CGT GGC TTG CCA GCC ATG GAT 702  
 Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro Ala Met Asp  
 170 175 180

	GAG CAG TCG ATG ACC TCT GAC CCA TAT ATC AAA ATG ACG ATC CTC CCA Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr Ile Leu Pro 185 190 195 200	750
5	GAG AAG AAG CAT AAA GTG AAA ACT AGA GTG CTG AGA AAA ACC TTG GAT Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr Leu Asp 205 210 215	798
10	CCA GCT TTT GAT GAG ACC TTT ACA TTC TAT GGG ATA CCC TAC ACC CAA Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Thr Gln 220 225 230	846
15	ATC CAA GAA TTG GCC TTG CAC TTC ACA ATT TTG AGT TTT GAC AGG TTT Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp Arg Phe 235 240 245	894
20	TCA AGA GAT GAT ATC ATT GGG GAA GTT CTA ATT CCT CTC TCG GGA ATT Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu Ser Gly Ile 250 255 260	942
	GAA TTA TCT GAA GGA AAA ATG TTA ATG AAT AGA GAG ATC ATC AAG AGA Glu Leu Ser Glu Gly Lys Met Leu Met Asn Arg Glu Ile Ile Lys Arg 265 270 275 280	990
25	AAT GTT AGG AAG TCT TCA GGA CGG GGT GAG TTA CTG ATC TCT CTC TGC Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu Leu Ile Ser Leu Cys 285 290 295	1038
30	TAT CAG TCC ACC ACA AAC ACT CTA ACT GTG GTT GTC TTA AAA GCT CGA Tyr Gln Ser Thr Thr Asn Thr Leu Thr Val Val Val Leu Lys Ala Arg 300 305 310	1086
35	CAT CTG CCT AAA TCT GAT GTG TCC GGA CTT TCA GAT CCC TAT GTC AAA His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser Asp Pro Tyr Val Lys 315 320 325	1134
40	GTG AAC CTG TAC CAT GCC AAA AAG AGA ATC TCC AAG AAG AAG ACT CAT Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser Lys Lys Lys Thr His 330 335 340	1182
	GTG AAG AAA TGC ACC CCC AAT GCA GTG TTC AAT GAG CTG TTT GTC TTT Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn Glu Leu Phe Val Phe 345 350 355 360	1230
45	GAT ATT CCT TGT GAG GGC CTT GAA GAT ATA AGT GTT GAA TTT TTG GTT Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser Val Glu Phe Leu Val 365 370 375	1278
50	TTG GAT TCT GAA AGG GGG TCC CGA AAT GAG GTA ATC GGG CAG TTA GTC Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu Val 380 385 390	1326
55	TTG GGT GCA GCA GCA GAA GGA ACT GGT GGA GAG CAC TGG AAA GAG ATC Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu Ile 395 400 405	1374
60	TGT GAC TAC CCC AGG AGA CAA ATT GCC AAG TGG CAC GTG CTC TGT GAT Cys Asp Tyr Pro Arg Arg Gln Ile Ala Lys Trp His Val Leu Cys Asp 410 415 420	1422
	GGT TAGCATCCTA GCCGTGAGTT GGAACCTAAA GGTTTTTACT AGGCAAGGAG Gly 425	1475
65	AAATTTTCTT TCTTTCTATA TTGGATTGCA AGCTTGGGAA ATCAAGCTAC CTTTTTGTTG TTGTTGTTGT TGCTAGAAAT GGATTGAATT AGTAGACCAG AAAGTAACTT CAAATGTGTA	1535 1595

	TTATGATAAT TTCCCTATTT ATTAGAAGAG TTGGATAAAT TTTCATAAGA TATTCAATAT	1655
	CTCCTTCAGA TTACCAGTGA TATAACTAGG AATAGTCAGA CATTTTATGA ATACTGTGCC	1715
5	AGAATCCCAA ATTATAAATG TGACAACTCTC ATTGGAACAT GTCACAAAAA GTTAATGTGA	1775
	TTAAGATTTA AAAACGAAAA GTATGCCTTG CCTTGTGAAA ATTTATCCAT TTATCTTCAG	1835
10	GTTGGGGGAA ATCAATTTTT CTTTAATCCA AAGATACTAA AAAAATGTCC TCCAGTTTGT	1895
	ATTTATTAAT TCTGTCATGT GCAAATGGTT GTCCTGCATA TAAAAGTATC TGGTCATTTT	1955
	AGTTTGGTTT GTAATTATTT GATGCAATTT TATCATAAGA GTAAGTCAGA TTCATTTCAA	2015
15	AAGGACAGTG AACAAGCTGA GAAATTATTT TATCAAAGGG CTGAGTTGAG AACACTGTGG	2075
	CTGAAATATA ATTTTCTCC CCCCTAAGGT TACATGTGAG TCAAAATTTT GTAAATATA	2135
20	ACCTCACATA AGAACCATGG CCTTGGATTA TTCACTGCCT GTCACAAGCC TCAGTGTGGC	2195
	CTGAGAAATC CCTATGTACC TTTGTGAAAT TGTTGAATTA GTTAGTGAAT AAAGAAATAA	2255
	ACTTCAACTA GAAATCCAGT TAGAAGTGCA ATTTTCTTAT AGGAAATAGG TATAGTGTGC	2315
25	AAGTGTACTT TTAAGGCCAT CGTTTGTACC CAGAGTCGGC ATGGCCACCT AAGTCTTCAT	2375
	TTAATTTATT GTCCCCCAGA AAAGATTAAG ATGCTACTTG AAAAGACTGT GAAGATTTTT	2435
30	TACATTGCCA GATAAAAAGT GTTACTTAAC CAACAAACAA ATGTAAGACT ACAAATCGT	2495
	TCAAGAGCAA TTCTAATATA ATTTACATAT GTTCACGCAA AATATGCTTA GGCTGTCAAA	2555
	TTAGCACAAC AAAGAATGTG TTTCACTATC TTTTCTAGGC TAATTTGTCT TGAGCTGTTG	2615
35	TCTATAGAGC AGTTTACAGA CTTGTGTCTT GTATCATTTT CCAGTGCCAG GGTTCTGAAA	2675
	TTCAATTCAGA ACCTGTTAGA TTAAAGCTGC ACCCTGTGAT TATTTGAAAA GAATTAGCTT	2735
40	GAGAGTAATG TCACTATATT TGAGTTCTTA GAGAAGTATG AGTGGAACCT GAGTACAGTT	2795
	GAATTATTAA ATATGCAAGT TAGAAATTAA GTCTACTGAA AAATTTACAT TTTGAGTCAG	2855
	GTTTTGTGTC AGTACTTTAG CAGTTTTTGA GAATGTGTTT GATATCACAG TGTTTGTA	2915
45	TTCTATGAAA AATGCATTTT CCAAACAAC TATACATGCT TTTTATGACT ATGCCTAATG	2975
	TAAAGAAAAT GTATTACATT CTGTATGTAC AAAGATTAAA AATCAACCTC TTTTTGTGC	3035
50	TTTAAAATGA CTTTGGGATT AAAAAAGCAT ATTTCCCAAT CATTGTCTTC ATTCCACTAC	3095
	AAAGTCACCT CACAGCATCT TGCTCCACTC GGCATCTCTG TGAAAGCAAC ATGAAATGAA	3155
	CTGTAGTAGG TGTGTAGTTT GGGGAAGTCA AATGGCCATT TTATGTATGT GCATTTGGTA	3215
55	TCATGGGCCG TGGAACAGAA TATATGTTGG ACCTCTGAAA AGTTGTAAGG GGCCAAATCT	3275
	AAGTATTCTT CACGGCAGCC AGAAGTTAAT GGTGGTAGCA GCTGAGGTAT GGTGTTGGA	3335
60	CGAGGCCGAT TTTTTTTTTT TAACATGGAA CAATGAAACC AACAACAAAC ATTTTAAAA	3395
	TTAAAATGGA TAATTTGTAA ATAGTTTTTA GCTTTTAAAA TTAAAGTGT TTTTGAGTGT	3455
	GAAAAGTTGA GTAAACTAT TTGCAACTGG TTTTCAGAAA AGAGAAAAGA AACAACAAAG	3515
65	GAATTGAAAC AGGCAGGGAG ATCTTAATAC CTAATTTTCA CATTCTGCA AAATGTACTG	3575
	TTTTAGAATG TATTACAATA TCAATGTGAA TATCTTGAAT CCTGTTACAA ATCCTGCACT	3635

	GTATTAAACA TGTAATTAA TTGTTTGTCT GATTAGCCAA TCTCACCACC CAAATGGGGA	3695
	GGTATACATG TTTGAAGAAC GTGTAACTCG GTAATTGATT TGTICTGATG TTGTAACCTCA	3755
5	ATAGAAGTGT TTTGGAAGGA AGCATGGTGT GTGAGACAGT GTCTGTTCTT TTGTGCCAGC	3815
	TCTGTATGAT GTTTGTAAGA CCATGTTTGT AAGACATGAA TAAATTGCTG CTTTTGCCCA	3875
10	AAAAAAAAAA AAAAAA	3891

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 425 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Pro Ile Thr Thr Ser Arg Glu Glu Phe Asp Glu Ile Pro Thr  
1 5 10 15

15 Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu  
20 25 30

Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr  
35 40 45

20 Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro  
50 55 60

25 Glu Asn Leu Asn Ser Lys Lys Lys Phe Gly Ala Asp Asp Lys Asn Glu  
65 70 75 80

Val Lys Asn Lys Pro Ala Val Pro Lys Asn Ser Leu His Leu Asp Leu  
85 90 95

30 Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro  
100 105 110

Gly Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu  
115 120 125

35 Gly Glu Lys Glu Ser Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser  
130 135 140

40 Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Phe Ser  
145 150 155 160

Leu Glu Tyr Asn Phe Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu  
165 170 175

45 Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro  
180 185 190

Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr  
195 200 205

50 Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr  
210 215 220

55 Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe  
225 230 235 240

Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu  
245 250 255

60 Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu  
260 265 270

Met Asn Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg  
275 280 285

65 Gly Glu Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu  
290 295 300

Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser  
 305 310 315 320  
 5 Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys  
 325 330 335  
 Arg Ile Ser Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala  
 340 345 350  
 10 Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu  
 355 360 365  
 Asp Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg  
 370 375 380  
 15 Asn Glu Val Ile Gly Gln Leu Val Leu Gly Ala Ala Ala Glu Gly Thr  
 385 390 395 400  
 20 Gly Gly Glu His Trp Lys Glu Ile Cys Asp Tyr Pro Arg Arg Gln Ile  
 405 410 415  
 Ala Lys Trp His Val Leu Cys Asp Gly  
 420 425